

FIG. 1

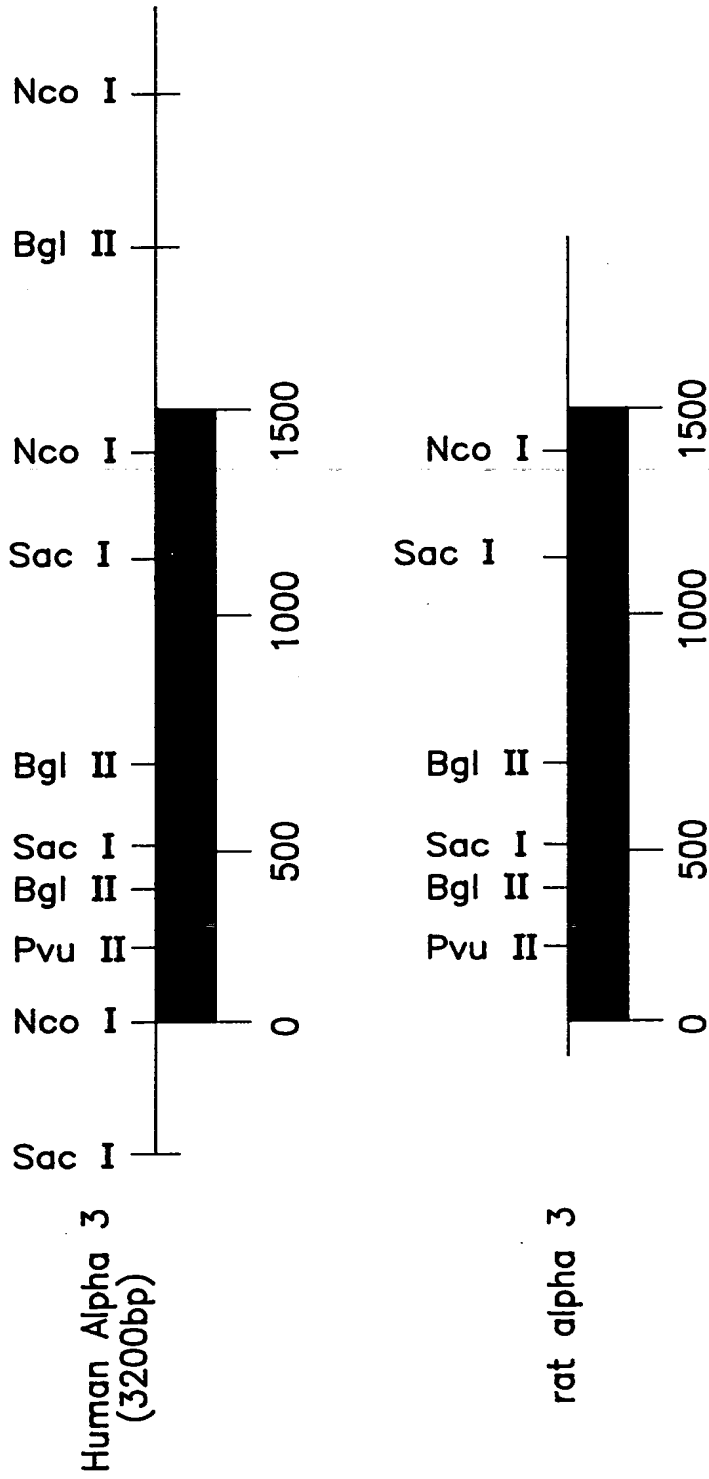


FIG. 2

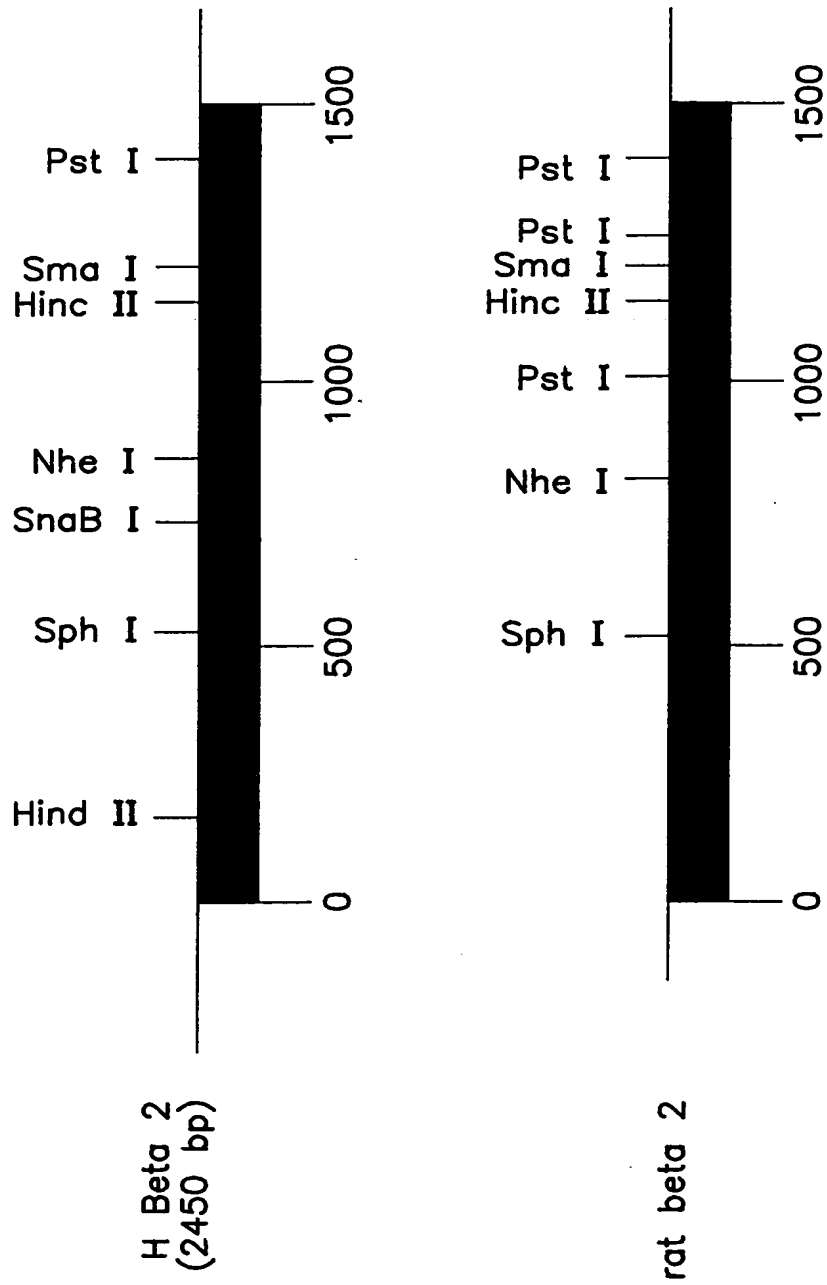


FIG. 3

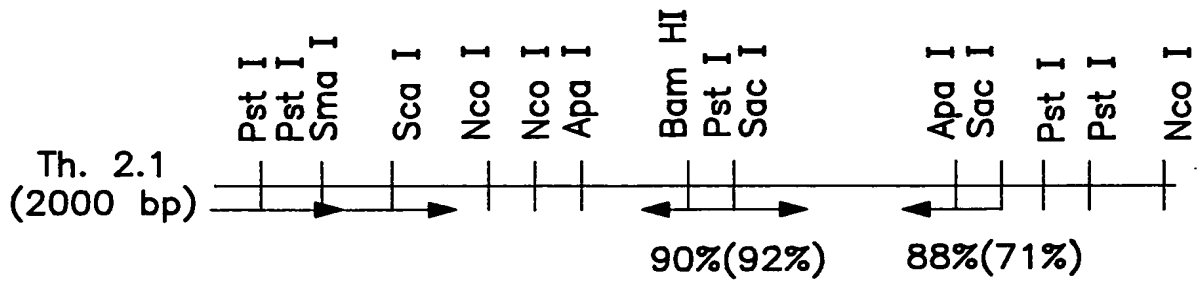


FIG. 4A

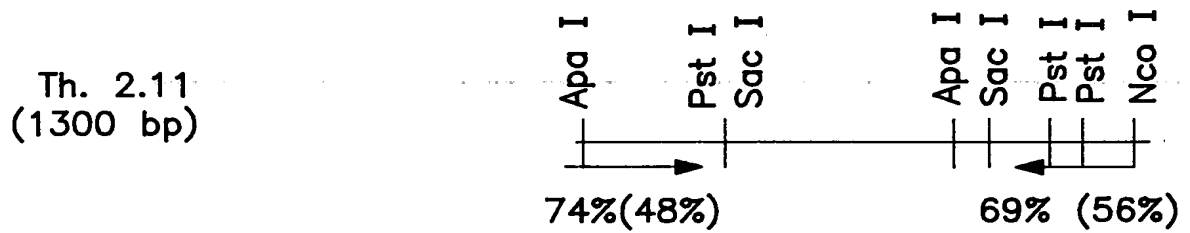


FIG. 4B

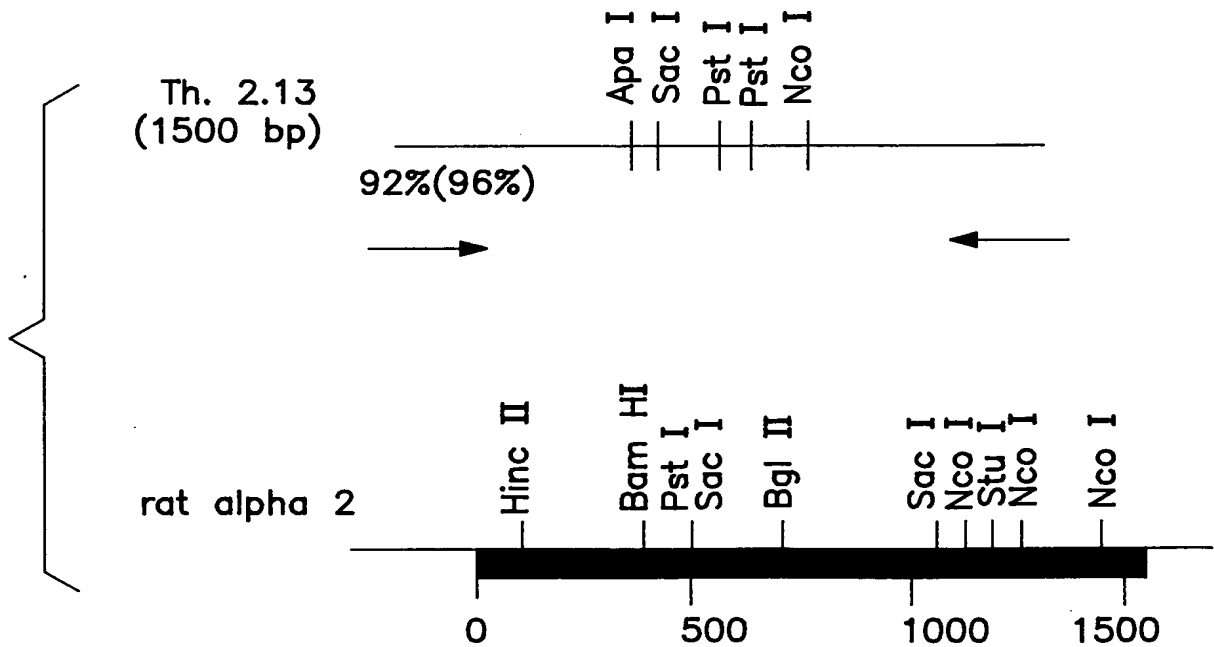


FIG. 4C

B.S. 3.3
(2500 bp)

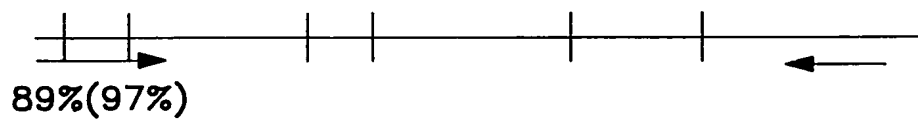
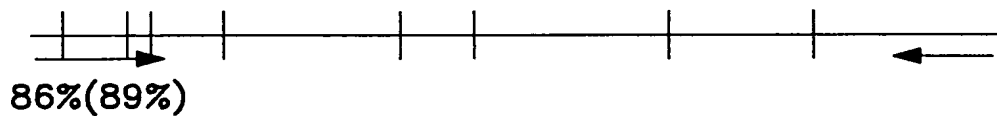


FIG. 5A

B.S. 3.5
(2800 bp)



rat alpha 3

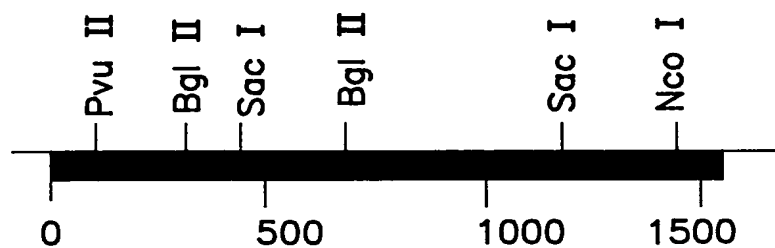


FIG. 5B

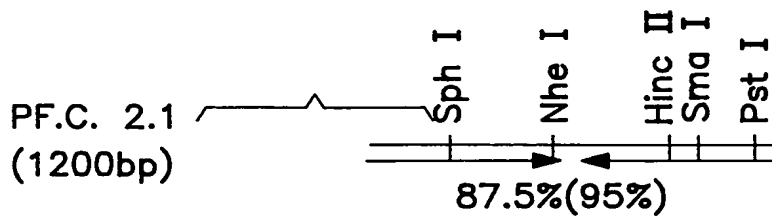


FIG. 6A

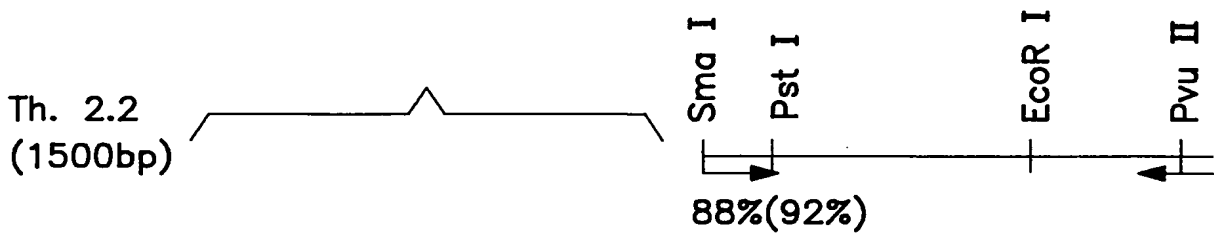


FIG. 6B

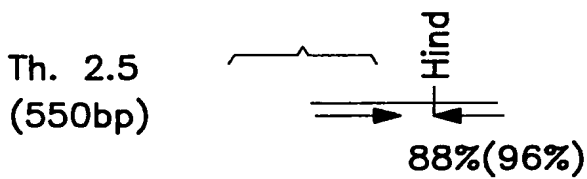


FIG. 6C

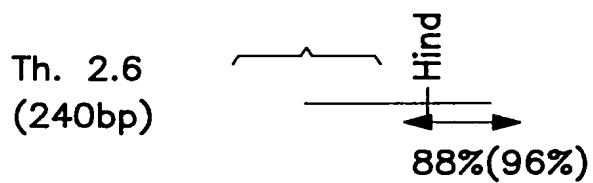


FIG. 6D

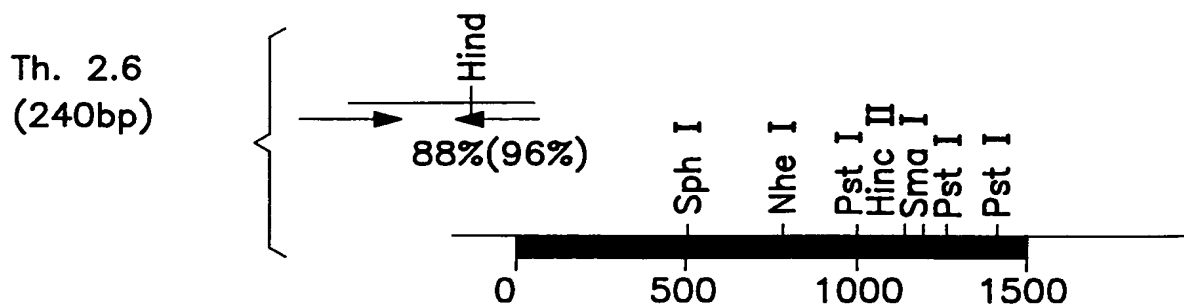


FIG. 6E

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195 .....GCTAAACAGGAGTGGAGCGACTACAAACTGCGCTGGAAC 157
      || ||||| |||| | ||||| ||||| ||||| ||||| |||||
251 CCAATGTCTGGCTAAAGCAGGAATGGAATGACTACAAGCTGCGCTGGGAC 300

156 CCCGCTGATTTTGGCAACATCACATCTCTCAGGGTCCCTTCTGAGATGAT 107
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 CCGGCTGAGTTTGGCAATGTCACCTCCCTGCGCGTCCCTTCAGAGATGAT 305

      BamHI
106 CTGGATCCCGGACATTGTTCTCTACAACAA...AAATGGGGAGTTTGCAG 60
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
351 CTGGATCCAGACATTGTCCTCTACAACAATGCAGATGGGGAGTTTGCAG 400

59 TGACCCACATGACCAAGGCCACCTCTTCTCCACGGGCACTGTGCACTGG 10
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
401 TGACCCACATGACCAAGGCTCACCTCTTCTTACGGGCACTGTGCACTGG 450

9  GTGCCCCC
   |||||
   |||||
451 GTGCCCCA

```

FIG. 7A

1 ATGCCCGCTGGCATGGCCCGGCGCTGCGGCCCGTGGCGCTGCTCCTTGG 50
 |||| | ||| ||||| ||| || | | ||||| || |
 |||| | ||| ||||| ||| || | | ||||| || |
 1 ATGCTGGCTTGCATGGCCGGGCACTCCAACCTCAATGGCGCTGTTC...AG 47

 51 CTTCCGGCCTCCTCCGGCTGTGCTCAGGGGTGTGGGTACGGATACAGAGG 100
 |||| | |||| || | ||||| ||||| ||| || | ||||| ||
 |||| | |||| || | ||||| ||||| ||| || | ||||| ||
 48 CTTCAGCCTTCTTTGGCTGTGCTCAGGGGTTTGGGAAGTACACAGAGG 97

 101 AGCGGCTGGTGGAGCATCTCCTGGATCCTTCCCGCTACAACAAGCTTATC 150
 ||||| ||||| ||||| ||| ||||| ||||| ||||| ||| ||
 ||||| ||||| ||||| ||| ||||| ||||| ||||| ||| ||
 98 AGCGGCTAGTGGAGCATCTCTTAGATCCCTCCCGCTATAACAAGCTGATT 147

 151 CGCCCAGCCACCAATGGCTCTGAGCTGGTGACAGTACAGCTTATGGTGTC 200
 || ||||| || || | ||||| ||||| ||||| ||||| ||| ||
 || ||||| || || | ||||| ||||| ||||| ||||| ||| ||
 148 CGTCCAGCTACTAACGGCTCTGAGCTGGTGACTGTACAGCTCATGGTATC 197

 201 ACTGGCCCAGCTCATCAGTGTGCATGAGCGGGAGCAGATCATGACCACCA 250
 | |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 | |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 198 ATTGGCTCAGCTCATTAGTGTGCACGAGCGGGAGCAGATCATGACCACCA 247

 251 ATGTCTGGCTGACCCAGGAGTGGGAAGATTATCGCCTCACCTGGAAGCCT 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 248 ATGTCTGGCTGACCCAGGAGTGGGAAGATTACCGCCTCACATGGAAGCCT 297

 301 GAAGAGTTTGACAACATGAAGAAAGTTCGGCTCCCTTCCAAACACATCTG 350
 || || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 || || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 248 GAGGACTTCGACAATATGAAGAAAGTTCGGCTCCCTTCCAAACACATCTG 347

FIG. 9A

701 TTCGCCGCAAGCCGCTCTTCTACACCATCAACCTCATCATCCCCTGTGTG 750
 |||| | |||| | | |||| |||| |||| |||| |||| |||| |||| ||||
 |||| | |||| | | |||| |||| |||| |||| |||| |||| |||| ||||
 698 TTCGTCGCAAACCACTCTTCTACACTATCAACCTCATCATCCCCTGCGTA 747

 751 CTCATCACCTCGCTAGCCATCCTTGTCTTCTACCTGCCATCCGACTGTGG 800
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 748 CTCATCACCTCGCTGGCCATCCTGGTCTTCTACCTGCCCTCAGACTGTGG 797

 801 CGAGAAGATGACGTTGTGCATCTCAGTGCTGCTGGCGCTCACGGTCTTCC 850
 || |||| |||| | || || || || |||| |||| || |||| |||| ||||
 || |||| |||| | || || || || |||| |||| || |||| |||| ||||
 798 TGAAAAGATGACACTTTGTATTTCTGTGCTGCTAGCACTCACGGTGTTC 847

 851 TGCTGCTCATCTCCAAGATCGTGCCTCCACCTCCCTCGACGTGCCGCTC 900
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 848 TGCTGCTCATCTCCAAGATTGTGCCTCCACCTCCCTCGATGTACCGCTG 897

 901 GTCGGCAAGTACCTCATGTTACCATGGTGCTTGTCACCTTCTCCATCGT 950
 || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 898 GTGGGCAAGTACCTCATGTTTACCATGGTGCTAGTCACCTTCTCCATCGT 947

 951 CACCAGCGTGTGCGTGCTCAACGTGCACCACCGCTCGCCCACCACGCACA 1000
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 948 CACCAGCGTGTGTGTGCTCAATGTGCACCACCGCTCGCCTACCACGCACA 997

 1001 CCATGGCGCCCTGGGTGAAGGTCGTCTTCCTGGAGAAGCTGCCC GCGCTG 1050
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 998 CCATGGCCCCCTGGGTCAAGGTGGTCTTCCTGGAGAAGCTGCCCACTG 1047

FIG. 9C

PstI

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1401 CTGGATCTTTGTCTTTGTCTGTGTCTTTGGCACCATCGGCATGTTCTCTGC 1450
      |||
1392 GTGGATCTTTGTCTTTGTCTGTGTCTTTGGGACCGTCGGCATGTTCTCTGC 1441
      |||

1451 AGCCTCTCTTCCAGAACTACACCACCACCACCTTCCTCCACTCAGACCAC 1500
      |||
1442 AGCCTCTCTTCCAGAACTACACTGCCACTACCTTCCTCCACCCTGACCAC 1491
      |||

1501 TCAGCCCCCAGCTCCAAGTGA 1521
      |||
1492 TCAGCTCCCAGCTCCAAGTGA 1512
      |||

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FIG. 9E